

Predictive toxicogenomics for the identification of chemical carcinogens : application to human hepatic cell lines

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Propositions

belonging to the dissertation:

Predictive toxicogenomics for the identification of chemical carcinogens: *Application to human hepatic cell lines*

by

Christina Magkoufopoulou
Maastricht, 8th December 2011

All models are approximations. Essentially, all models are wrong, but some are useful. However, the approximate nature of the model must always be borne in mind.

G.E.P. Box, N.R. Draper

Gene expression levels of HepaRG cells closely resemble those observed in human hepatocytes and human liver *in vitro*.

This thesis - Chapter 2

For the identification of genotoxic carcinogens, gene expression profiles induced in HepG2 cells by chemical agents perform better than those induced in HepaRG cells.

This thesis - Chapter 2

Evaluation of gene expression alterations induced in HepG2 cells by chemical agents facilitates the identification of false positive results from standard *in vitro* genotoxicity assays.

This thesis - Chapter 3

Transcriptomics approaches will overlook essential information, unless all possible functions of all known genes are fully elucidated.

This thesis - Chapter 5

Going from a whole genome to just a few sentinel genes is proof that the circle [of the microarrays era] is closing.

J.M. Garcia-Sagredo

The combination of Ames bacterial mutagenicity assay with specific gene expression alterations in HepG2 cells provides a novel and highly accurate *in vitro* genotoxicity test battery.

This thesis - Chapter 4

Given a large mass of data, we can by judicious selection construct perfectly plausible unassailable theories — all of which, some of which, or none of which may be right.

P.A. Srere

It is a capital mistake to theorize before one has data. Insensibly one begins to twist facts to suit theories, instead of theories to suit facts.

A.C. Doyle